

In the Claims

Please amend the claims by replacing all prior versions of the claims pursuant to 37 C.F.R. §1.121 as modified by 68 Fed. Reg. 38611 (June 30, 2003) as indicated below.

The claims are marked to show differences relative to the claims pending as of the January 30, 2004 final Office Action.

1. (Currently Amended) A method of modifying the content or composition, or content and composition, of a metabolite in the seed of a plant comprising:

- (i) ~~expressing in the seed of the~~ introducing into a plant a chimeric gene comprising a nucleotide sequence encoding a sunflower seed albumin protein placed operably in connection with a promoter sequence capable of conferring expression in the seed wherein the nucleotide sequence is expressed in the seed; and
- (ii) determining the content or composition, or content and composition, of a metabolite in the seed, said metabolite selected from the group consisting of fatty acid, starch, soluble non-starch polysaccharide, insoluble non-starch polysaccharide, fibre and total protein nitrogen, ~~and~~
- ~~(iii) selecting a~~ wherein the plant having has a modified content or composition, or content and composition, of a metabolite in the seed thereof, as compared to a plant in which said chimeric gene is not expressed, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

2-4. (Canceled)

5. (Previously presented) The method according to claim 1 wherein the total protein nitrogen content is increased.
6. (Previously presented) The method according to claim 1 wherein the fibre content or composition is modified.
7. (Canceled)
8. (Previously presented) The method according to claim 1 wherein the fatty acid content is increased or decreased.
- 9-13. (Canceled)
14. (Previously presented) The method according to claim 1 wherein the plant is a dicotyledonous plant.
15. (Previously presented) The method according to claim 14 wherein the dicotyledonous plant is a pea or chickpea plant.
16. (Previously presented) The method according to claim 1 wherein the promoter sequence comprises the pea vicilin gene promoter sequence.
17. (Previously presented) The method according to claim 1 wherein the plant is a monocotyledonous plant.
18. (Original) The method according to claim 17 wherein the monocotyledonous plant is a rice plant.
19. (Previously presented) The method according to claim 1 wherein the promoter ~~comprises a~~ sequence is a *Triticum aestivum* HMW glutenin promoter sequence.
20. (Previously presented) The method according to claim 1 further comprising the first steps of:

- (i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and
- (ii) regenerating an intact plant therefrom.

21. (Currently Amended) A method of increasing the total protein nitrogen content of seeds of a plant, said method comprising

- (i) ~~expressing in the seeds of the~~ introducing into a plant a chimeric gene comprising a nucleotide sequence encoding a sunflower seed albumin protein placed operably in connection with a promoter sequence capable of conferring expression in ~~said the~~ seeds, said nucleotide sequence also positioned upstream of a transcription termination sequence wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining the content of total protein nitrogen in the seeds; and
- ~~(iii) selecting a wherein the plant having~~ has an increased total protein nitrogen content in the seeds thereof as compared to the seeds of a plant which does not express the chimeric gene, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

22. (Original) The method according to claim 21 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

23. (Original) The method according to claim 21 wherein the ~~chimeric gene further comprises promoter sequence~~ is the pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription terminator sequence.

24. (Previously presented) The method according to claim 22 wherein the plant is pea or chickpea.

25. (Original) The method according to claim 21 wherein the promoter sequence is a wheat HMW glutenin gene promoter and the plant is a monocotyledonous plant.
26. (Original) The method according to claim 21 wherein the ~~chimeric gene further comprises~~ promoter sequence is the wheat HMW glutenin gene promoter and/or the transcription termination sequence NOS transcription terminator sequence.
27. (Previously presented) The method according to claim 25 wherein the plant is a rice plant.
28. (Currently Amended) A method of increasing or decreasing fatty acid content of seeds of a plant, said method comprising:
- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds wherein the nucleotide sequence is expressed in the seeds; and
 - (ii) determining the content of a fatty acid in the seed; and
 - ~~(iii) selecting a wherein the plant having~~ has increased or decreased content of the fatty acid in the seeds thereof as compared to the seeds of a plant which does not express the chimeric gene, ~~and~~ wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.
29. (Original) The method according to claim 28 wherein the promoter sequence is the pea vicilin gene promoter and the

plant is a dicotyledonous plant.

30. (Original) The method according to claim 28 wherein the ~~chimeric gene further comprises~~ promoter sequence is the pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription terminator sequence.
31. (Canceled)
32. (Previously presented) The method according to claim 29 wherein if the plant is pea the content of fatty acids in the seeds is decreased.
33. (Currently Amended) A method of modifying the fatty acid composition of seeds of a plant, said method comprising
- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
 - (ii) determining the fatty acid composition of the seeds; and
 - (iii) ~~selecting a~~ wherein the plant having has a modified fatty acid composition in the seeds thereof, as compared to seeds of a plant in which the chimeric gene is not expressed, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.
34. (Original) The method according to claim 33 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

35. (Original) The method according to claim 33 wherein the ~~chimeric gene further comprises promoter sequence is the~~ pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription terminator sequence.
36. (Canceled)
37. (Previously presented) The method according to claim 33 wherein the fatty acid is selected from the group consisting of: myristic acid, stearic acid, gadoleic acid, behenic acid, lignoceric acid, oleic acid, linoleic acid, linolenic acid and erucic acid.
38. (Currently Amended) A method of decreasing the starch content of seeds of a plant, said method comprising:
- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
 - (ii) determining the starch content of the seeds; and
 - ~~(iii) selecting a wherein the plant having has~~ a decreased starch content in the seeds thereof, as compared with seeds of a plant in which the chimeric gene is not expressed, and wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.
39. (Original) The method according to claim 38 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

40. (Original) The method according to claim 38 wherein the ~~chimeric gene further comprises promoter sequence is~~ the pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription terminator sequence.
41. (Previously presented) The method according to claim 39 wherein the plant is a pea plant.
42. (Currently Amended) A method of modifying the amino acid composition of seeds of a plant, said method comprising:
- (1) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and
 - (ii) determining the amino acid composition of the seeds; and
 - ~~(iii) selecting a~~ wherein the plant having has a modified amino acid composition in the seeds thereof, as compared to a plant in which the chimeric gene is not expressed, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.
43. (Original) The method according to claim 42 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.
44. (Original) The method according to claim 42 wherein the ~~chimeric gene further comprises promoter sequence is~~ the pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription

terminator sequence.

45. (Previously presented) The method according to claim 43 wherein the plant is pea or chickpea.

46. (Original) The method according to claim 45 wherein the proportion of arginine relative to other amino acids is increased.

47. (Currently Amended) A method of increasing or decreasing the fibre content of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining the fibre content of the seeds; and
- ~~(iii) selecting a~~ wherein the plant having has an increased or a decreased content of fibre in the seeds thereof, as compared with seeds of a plant which does not express said chimeric gene, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

48. (Original) The method according to claim 47 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

49. (Original) The method according to claim 47 wherein the ~~chimeric gene further comprises~~ promoter sequence is the pea vicilin gene promoter sequence and the transcription

termination sequence is a vicilin gene transcription terminator sequence.

50. (Canceled)

51. (Previously presented) The method according to claim 48 wherein if the plant is a pea plant the content of fibre in the seed is increased.

52. (Currently Amended) A method of modifying the fibre composition of seeds of a plant, said method comprising:

- (i) ~~the step of expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining the fibre composition of the seeds; and
- (iii) ~~selecting a~~ wherein the plant having has a modified fibre composition in the seeds thereof, as compared with seeds of a plant in which the chimeric gene is not expressed, and
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

53. (Original) The method according to claim 52 wherein the promoter sequence is the pea vicilin gene promoter and the plant is a dicotyledonous plant.

54. (Original) The method according to claim 53 wherein the ~~chimeric gene further comprises promoter sequence~~ is the pea vicilin gene promoter sequence and the transcription termination sequence is a vicilin gene transcription

terminator sequence.

55. (Canceled)

56. (Currently Amended) The method according to claim 52 wherein the content of soluble non-starch polysaccharide, or the content of insoluble non-starch polysaccharide, or the content of both in the seed is decreased.

57. (Currently Amended) The method according to claim 52 wherein the content of lignin in the seed is increased.

58-63. (Canceled)

64. (Previously Presented) The method according to any one of claims 21, 28, 33, 38, 42, 47, or 52 further comprising the first steps of:

- (i) introducing the chimeric gene into a plant cell, tissue, organ or whole organism; and
- (ii) regenerating an intact plant therefrom.

65. (Currently Amended) A transformed plant having a modified content or composition, or content and composition, of a metabolite in its seed, wherein the modification is by the method according to any one of claims 1, 21, 28, 33, 38, 42, 47, 52, or 102, or progeny of ~~said the~~ plant, wherein ~~said the plant or the~~ progeny comprises ~~at least one copy of the chimeric gene~~ a chimeric gene comprising a nucleotide sequence encoding a sunflower seed albumin protein in an expressible format, and wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

66. (Canceled)

67. (Previously presented) A seed derived from the plant according to claim 65 wherein said seed comprises at least one copy of the chimeric gene in an expressible format.
68. (Canceled)
69. (Original) The seed derived from the transformed plant of claim 65, wherein the seed has a modified content or composition, or content and composition of a metabolite, wherein the modification is at least one of:
- a) increased total protein nitrogen content;
 - b) decreased total starch content;
 - c) increased or decreased fatty acid content;
 - d) modified fatty acid composition;
 - e) increased or decreased fibre content; or
 - f) modified fibre composition.
- 70-87. (Canceled)
88. (Currently Amended) The method of claim 1 wherein the total protein nitrogen content of the seed is increased.
89. (Currently Amended) The method of claim 1 wherein the amino acid composition of the seed is modified.
90. (Currently Amended) The method of claim 1 wherein ~~expression of the chimeric gene in the seed increases or decreases~~ the fibre content of the seed is increased or decreased.
91. (Currently Amended) The method of claim 1 ~~or claim 102~~ wherein ~~expression of the chimeric gene in the seed~~ modifies the fibre composition of the seed is modified.
92. (Currently Amended) The method of claim 1 wherein ~~expression of the chimeric gene in the seed decreases~~ the

total starch content of the seed is decreased.

93. (Currently Amended) The method of claim 1 wherein ~~expression of the chimeric gene in the seed increases or decreases~~ the total fatty acid content of the seed is increased or decreased.
94. (Currently Amended) The method of claim 1 wherein ~~expression of the chimeric gene in the seed~~ modifies the fatty acid composition of the seed is modified.
95. (Canceled)
96. (Currently Amended) The method of claim 1 wherein the chimeric gene further comprises a promoter sequence which confers strong expression at least in the seeds of the plant.
97. (Previously presented) The method according to claim 96 wherein the promoter is the pea vicilin promoter.
98. (Previously presented) The method according to claim 96 wherein the promoter is the wheat HMW glutenin promoter.
99. (Previously presented) The method of claim 96 wherein the chimeric gene further comprises a transcription terminator sequence placed downstream of the sequence encoding SSA.
100. (Previously presented) The method of claim 99 wherein the transcription terminator sequence is the pea vicilin gene terminator sequence.
101. (Currently Amended) The method according to claim 1 or ~~claim 102~~, wherein the content or composition, or content and composition, of more than one metabolite in the seed of the plant is modified.

~~102. (Currently Amended) A method of modifying the content or composition, or content and composition, of a metabolite in the seed of a plant comprising:~~

- ~~(i) expressing in the seed of the plant a chimeric gene comprising a nucleotide sequence encoding a sunflower seed albumin protein placed operably in connection with a promoter sequence capable of conferring expression in the seed; and~~
- ~~(ii) determining whether the content or composition, or content and composition, of a metabolite in the seed of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.~~

103. (Currently Amended) A method of increasing the total protein nitrogen content of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of the~~ introducing into a plant a chimeric gene comprising a nucleotide sequence encoding a sunflower seed albumin protein placed operably in connection with a promoter sequence capable of conferring expression in said seeds, said nucleotide sequence also positioned upstream of a transcription termination sequence wherein the nucleotide sequence is expressed in the seed; and
- (ii) determining whether the content of total protein nitrogen in the seeds of the plant is increased as compared to that of a plant in which the chimeric gene is not expressed,
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

104. (Currently Amended) A method of increasing or decreasing the

fatty acid content of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining whether the content of a fatty acid in the seeds of the plant is increased or decreased as compared to that of a plant in which the chimeric gene is not expressed,
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

105. (Currently Amended) A method of modifying the fatty acid composition of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining whether the fatty acid composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed,
wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

106. (Currently Amended) A method of decreasing the starch content of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining whether the starch content of the seeds of the plant is decreased as compared to that of a plant in which the chimeric gene is not expressed, wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

107. (Currently Amended) A method of modifying the amino acid composition of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant; and
- (ii) determining whether the amino acid composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed, wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

108. (Currently Amended) A method of increasing or decreasing the fibre content of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed

upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and

- (ii) determining whether the fibre content of the seeds of the plant is increased or decreased as compared to that of a plant in which the chimeric gene is not expressed, wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

109. (Currently Amended) A method of modifying the fibre composition of seeds of a plant, said method comprising:

- (i) ~~expressing in the seeds of said~~ introducing into a plant a chimeric gene that comprises a structural gene sequence encoding sunflower seed albumin (SSA) placed upstream of a transcription termination sequence and operably in connection with a promoter sequence capable of conferring expression on said structural gene in the seeds of said plant wherein the nucleotide sequence is expressed in the seeds; and
- (ii) determining whether the fibre composition of the seeds of the plant is modified as compared to that of a plant in which the chimeric gene is not expressed, wherein the plant is wheat, oats, maize, barley, rice, sorghum, millet, rye, safflower, sunflower, soybean, pea, bean, lentil, or chickpea.

110. (Currently Amended) The method according to claim 1, wherein the total protein nitrogen content of the seed of the plant is increased by at least 10%.

111. (Canceled)

~~112. (Currently Amended) The method according to claim 1, wherein~~

~~the total fibre content of the seed of the plant is increased or decreased by at least 5%.~~

~~113. (Currently Amended) The method according to claim 1, wherein the total starch content of the seed of the plant is reduced by at least 10%.~~

~~114. (Currently Amended) The method according to claim 1, wherein the total fatty acid content of the seed of the plant is increased or decreased by at least 5%.~~

~~115. (Currently Amended) The method according to claim 1, wherein the content of any one fatty acid in the seed of the plant is increased or decreased by at least 5%.~~